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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/004,176

DATE: 12/14/2001

TIME: 11:09:06

Input Set : A:\Sequence Listing-2.txt

Output Set: N:\CRF3\12142001\I004176.raw

ENTERED

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3 <110> APPLICANT: Pang, Danny Z.
W--> 4 <120> TITLE OF INVENTION: Use of decorin in a cosmetic or dermatological composition
C--> 5 <140> CURRENT APPLICATION NUMBER: US/10/004,176
C--> 5 <141> CURRENT FILING DATE: 2001-11-02
W--> 5 <160> NUMBER OF SEQ ID: 6
W--> 0 <130> FILE REFERENCE:
      6 <170> SOFTWARE: PatentIn ver. 2.0
      8 <210> SEQ ID NO: 1
      9 <211> LENGTH: 28
     10 <212> TYPE: DNA
     11 <213> ORGANISM: Artificial Sequence
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     12 <223> OTHER INFORMATION: Synthetic Primer
W--> 13 <400> SEQUENCE: 1
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     17 <210> SEQ ID NO: 2
     18 <211> LENGTH: 30
     19 <212> TYPE: DNA
     20 <213> ORGANISM: Artificial Sequence
W--> 21 <220> FEATURE:
     21 <223> OTHER INFORMATION: Synthetic Primer
W--> 22 <400> SEQUENCE: 2
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     27 <211> LENGTH: 20
     28 <212> TYPE: DNA
     29 <213> ORGANISM: Artificial Sequence
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     30 <223> OTHER INFORMATION: Synthetic Primer
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     35 <210> SEQ ID NO: 4
     36 <211> LENGTH: 20
     37 <212> TYPE: DNA
     38 <213> ORGANISM: Artificial Sequence
W--> 39 <220> FEATURE:
     39 <223> OTHER INFORMATION: Synthetic Primer
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     45 <211> LENGTH: 990
     46 <212> TYPE: DNA
     47 <213> ORGANISM: Human
     48 <221> NAME/KEY: CDS
     49 <222> LOCATION: 1...990
W--> 50 <400> SEQUENCE: 5
     51 gtt gag gct tct ggg ata ggc cca gaa gtt cct gat gac cgc gac ttc 48

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52 Val Glu Ala Ser Gly Ile Gly Pro Glu Val Pro Asp Asp Arg Asp Phe
53   1          5          10          15
55 gag ccc tcc cta ggc cca gtg tgc ccc ttc cgc tgt caa tgc cat ctt 96
56 Glu Pro Ser Leu Gly Pro Val Cys Pro Phe Arg Cys Gln Cys His Leu
57          20          25          30
59 cga gtg gtc cag tgt tct gat ttg ggt ctg gac aaa gtg cca aag gat 144
60 Arg Val Val Gln Cys Ser Asp Leu Gly Leu Asp Lys Val Pro Lys Asp
61          35          40          45
63 ctt ccc cct gac aca act ctg cta gac ctg caa aac aac aaa ata acc 192
64 Leu Pro Pro Asp Thr Thr Leu Leu Asp Leu Gln Asn Asn Lys Ile Thr
65          50          55          60
67 gaa atc aaa gat gga gac ttt aag aac ctg aag aac ctt cac gca ttg 240
68 Glu Ile Lys Asp Gly Asp Phe Lys Asn Leu Lys Asn Leu His Ala Leu
69 65          70          75          80
71 att ctt gtc aac aat aaa att agc aaa gtt agt cct gga gca ttt aca 288
72 Ile Leu Val Asn Asn Lys Ile Ser Lys Val Ser Pro Gly Ala Phe Thr
73          85          90          95
75 cct ttg gtg aag ttg gaa cga ctt tat ctg tcc aag aat cag ctg aag 336
76 Pro Leu Val Lys Leu Glu Arg Leu Tyr Leu Ser Lys Asn Gln Leu Lys
77          100          105          110
79 gaa ttg cca gaa aaa atg ccc aaa act ctt cag gag ctg cgt gcc cat 384
W--> 80 Glu Leu Pro Blu Lys Met Pro Lys Thr Leu Gln Glu Leu Arg Ala His
81          115          120          125
83 gag aat gag atc acc aaa gtg cga aaa gtt act ttc aat gga ctg aac 432
84 Glu Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn Gly leu Asn
85          130          135          140
87 cag atg att gtc ata gaa ctg ggc acc aat ccg ctg aag agc tca gga 480
88 Gln Met Ile Val Ile Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser Gly
89 145          150          155          160
91 att gaa aat ggg gct ttc cag gga atg aag aag ctc tcc tac atc cgc 528
92 Ile Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg
93          165          170          175
95 att gct gat acc aat atc acc agc att cct caa ggt ctt cct cct tcc 576
96 Ile Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser
97          180          185          190
99 ctt acg gaa tta cat ctt gat ggc aac aaa atc agc aga gtt gat gca 624
100 Leu Thr Glu Leu His Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala
101          195          200          205
103 gct agc ctg aaa gga ctg aat aat ttg gct aag ttg gga ttg agt ttc 672
104 Ala Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe
105          210          215          220
107 aac agc atc tct gct gtt gac aat ggc tct ctg gcc aac acg cct cat 720
108 Asn Ser Ile Ser Ala Val Asp Asn Gly Ser Leu Ala Asn Thr Pro His
109 225          230          235          240
111 ctg agg gag ctt cac ttg gac aac aac aag ctt acc aga gta cct ggt 768
112 Leu Arg Glu Leu His Leu Asp Asn Asn Lys Leu Thr Arg Val Pro Gly
113          245          250          255
115 ggg ctg gca gag cat aag tac atc cag gtt gtc tac ctt cat aac aac 816
116 Gly Leu Ala Glu His Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn

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117          260          265          270
119 aat atc tct gta gtt gga tca agt gac ttc tgc cca cct gga cac aac      864
120 Asn Ile Ser Val Val Gly Ser Ser Asp Phe Cys Pro Pro Gly His Asn
121          275          280          285
123 acc aaa aag gct tct tat tgc ggt gtg agt ctt ttc agc aac cgc gtc      912
124 Thr Lys Lys Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro Val
125          290          295          300
127 cag tac tgg gag ata cag cca tcc acc ttc aga tgt gtc tac gtg cgc      960
128 Gln Tyr Trp Glu Ile Gln Pro Ser Thr Phe Arg Cys Val Tyr Val Arg
129 305          310          315          320
131 tct gcc att caa ctc gga aac tat aag taa      990
132 Ser Ala Ile Gln Leu Gly Asn Tyr Lys
133          325
137 <210> SEQ ID NO: 6
138 <211> LENGTH: 329
139 <212> TYPE: PRT
140 <213> ORGANISM: Human
W--> 141 <400> SEQUENCE: 6
143 Val Glu Ala Ser Gly Ile Gly Pro Glu Val Pro Asp Asp Arg Asp Phe
144 1          5          10          15
146 Glu Pro Ser Leu Gly Pro Val Cys Pro Phe Arg Cys Gln Cys His Leu
147          20          25          30
149 Arg Val Val Gln Cys Ser Asp Leu Gly Leu Asp Lys Val Pro Lys Asp
150          35          40          45
152 Leu Pro Pro Asp Thr Thr Leu Asp Leu Gln Asn Asn Lys Ile Thr
153          50          55          60
155 Glu Ile Lys Asp Gly Asp Phe Lys Asn Leu Lys Asn Leu His Ala Leu
156 65          70          75          80
158 Ile Leu Val Asn Asn Lys Ile Ser Lys Val Ser Pro Gly Ala Phe Thr
159          85          90          95
161 Pro Leu Val Lys Leu Glu Arg Leu Tyr Leu Ser Lys Asn Gln Leu Lys
162          100          105          110
164 Glu Leu Pro Glu Lys Met Pro Lys Thr Leu Gln Glu Leu Arg Ala His
165          115          120          125
167 Glu Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn Gly Leu Asn
168          130          135          140
170 Gln Met Ile Val Ile Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser Gly
171 145          150          155          160
173 Ile Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg
174          165          170          175
176 Ile Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser
177          180          185          190
179 Leu Thr Glu Leu His Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala
180          195          200          205
182 Ala Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe
183          210          215          220
185 Asn Ser Ile Ser Ala Val Asp Asn Gly Ser Leu Ala Asn Thr Pro His
186 225          230          235          240
188 Leu Arg Glu Leu His Leu Asp Asn Asn Lys Leu Thr Arg Val Pro Gly

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```

189           245           250           255
191 Gly Leu Ala Glu His Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn
192           260           265           270
194 Asn Ile Ser Val Val Gly Ser Ser Asp Phe Cys Pro Pro Gly His Asn
195           275           280           285
197 Thr Lys Lys Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro Val
198           290           295           300
200 Gln Tyr Trp Glu Ile Gln Pro Ser Thr Phe Arg Cys Val Tyr Val Arg
201 305           310           315           320
203 Ser Ala Ile Gln Leu Gly Asn Tyr Lys
204           325

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VERIFICATION SUMMARY

DATE: 12/14/2001

PATENT APPLICATION: US/10/004,176

TIME: 11:09:07

Input Set : A:\Sequence Listing-2.txt

Output Set: N:\CRF3\12142001\I004176.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:270 C: Current Application Number differs, Replaced Current Application No
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:5 M:283 W: Missing Blank Line separator, <160> field identifier
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:12 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:13 M:283 W: Missing Blank Line separator, <400> field identifier
L:21 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:22 M:283 W: Missing Blank Line separator, <400> field identifier
L:30 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:31 M:283 W: Missing Blank Line separator, <400> field identifier
L:39 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:40 M:283 W: Missing Blank Line separator, <400> field identifier
L:50 M:283 W: Missing Blank Line separator, <400> field identifier
L:80 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:141 M:283 W: Missing Blank Line separator, <400> field identifier